



**Organization:** Clemson University

**Title:** Development and Experimental Verification of Surface Effects in a Fluidics Model    **MTO**    **Simbiosys**

**Start Date:** June 2001

**End Date:** June 2004

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### Project Goals

This collaborative project between Clemson University and CFD Research Corporation is aimed at understanding and quantifying how MEMS surfaces, modified using controlled surface modification strategies, interact with biological fluids using surface analytical tools, standard bioassays and advanced computational surface deposition models. Specific goals are to:

- Use self-assembled monolayers (SAMS) as well-characterized templates to mimic surfaces found in MEMS devices and biological systems
- Measure adsorption of different biomolecules on SAMS-modified surfaces under static/flowing conditions using quantitative surface analytical methods/bioassays
- Develop high-fidelity computational models to simulate monolayer/multilayer biomolecular surface adsorption in complex geometries for static/flow conditions
- Use experimental data and models synergistically for: (a) parameter extraction; (b) model validation
- Use extracted data and validated model to develop design rules for biocompatible MEMS and microfluidics devices in which adverse effects of biofluids on device performance are avoided.

### Technical Approach

- Task 1: The test-bed technology will be microchannels that can be assembled, have fluid passed through, and be disassembled; the surface can then be re-analyzed to determine the effects of biological fluid interaction with the modified surface under flow/static conditions. The variable test-bed parameters will be channel diameter, geometry, surface roughness, composition, etc. We will look at biological fluids from single component systems (e.g. serum albumin or horseradish peroxidase in saline) to more complex fluids (blood, serum). We will use standard assays to determine whether or not the proteins remain functional after adsorption. We will determine the extent of these interactions using surface analysis combined with standard biological assays such as immunolabeling and SDS-PAGE to locate and quantify the extent of deposition. By testing these controlled surface modification strategies, we should be able to identify acceptable surface compositions for generating the data for creating the design rules.
- Task 2: Detailed computational sensitivity studies will be performed on input parameters (reaction rate constants, diffusivities, etc.) for existing (baseline) high-fidelity phenomenological protein-surface interaction models. Carefully designed experiments under static/flow conditions in simplified channel geometries with different protein-surface pairs involving various surface types (hydrophobic, cationic, etc.) will provide data for parameter extraction and model calibration. The effects of variations in temperature, pH and solution salt concentration on biomolecular binding affinities will be examined. Improved models for surface diffusion and interactions of solution-phase proteins with adsorbed proteins (native phase, denatured) will also be developed, calibrated and validated. We will also develop simplified reduced-order semi-empirical models to predict the occurrence of phenomena such as channel clogging. Finally, based upon insights and data from the detailed simulations, rules for the design of complex microfluidic systems, being in contact with bio-fluids, will be developed.

### Recent Accomplishments

- New Start

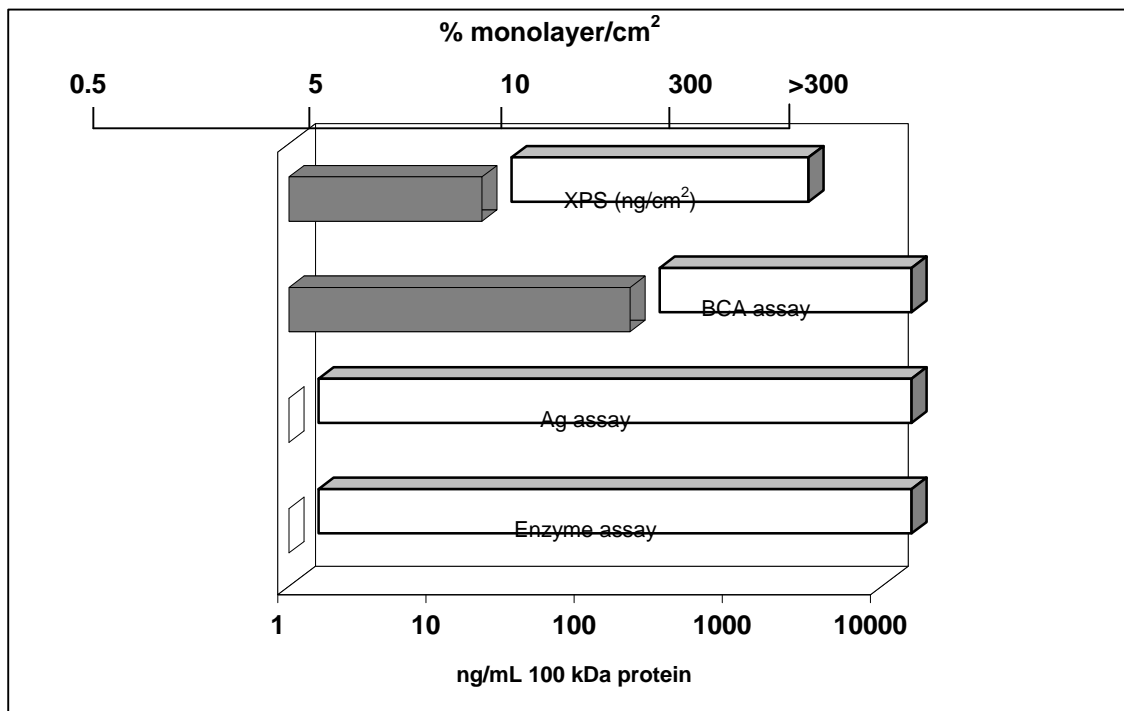
### Six-Month Milestones

- Selection of primary input parameters for baseline model based on sensitivity/experimental studies.

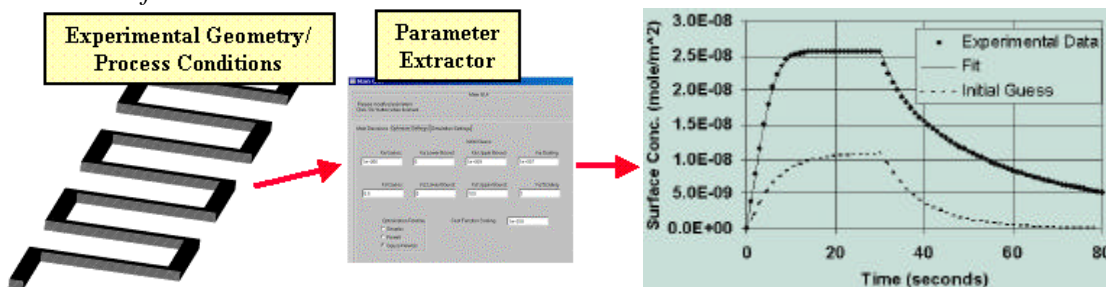
### Team Member Organizations

CFD Research Corporation

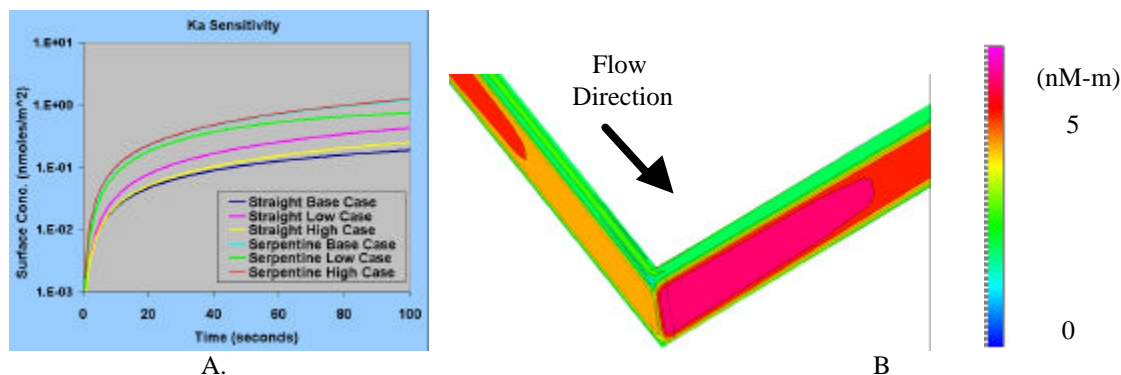
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**Figure 1:** Protein response ranges for the various analytical techniques validated on the project to date. The ranges are based on the experimental analysis metrics employed in our systems. For XPS; surface area of 1 cm<sup>2</sup>; BCA and Ag assays a protein solution volume of 100 mL and the enzyme assay is for a solution volume of 40 mL.



**Figure 2:** Automated Model Parameter Extraction Methodology from Surface Coverage Data



**Figure 3:** Model sensitivity studies: (A) Effect of adsorption rate constant on surface coverage in straight/serpentine channels; (B) Biomolecular surface coverage contours in serpentine channel